

makes it possible to amplify sequences specific to certain families and species, and to identify the organisms of these families or species.

Please amend the paragraph beginning at page 22, line 20, as follows:

Analysis of the amplificates makes it possible to show that it is possible to amplify, using the primers SEQ ID [[No.]] NO: 32 and SEQ ID [[No.]] NO: 33, the intergenic region of various Enterobacteria, such as *Escherichia coli*, *Enterobacter clocae*, *Morganella morganii*, *Serratia liquefaciens*, *Proteus mirabilis*, *Serratia marcescens*, *Klebsiella pneumoniae*, *Citrobacter freundii* or *Klebsiella oxytoca*. The amplified region varies in length, according to species, from 400 to 500 base pairs (bp). Use of the pair SEQ ID [[No.]] NO: 34 and SEQ ID [[No.]] NO: 36 gives amplificates of between 550 and 650 bp in length.

Please amend the paragraph beginning at page 23, line 4, as follows:

Analysis of the amplificates makes it possible to show that it is possible to amplify, using the pair of primers SEQ ID [[No.]] NO: 53 and SEQ ID [[No.]] NO: 54, the intergenic region of the various bacteria, such as *Escherichia coli*, *Clostridium leptum*, *Klebsiella oxytoca*, *Lactococcus lactis*, *Citrobacter freundii*, *Serratia marcescens*, *Proteus mirabilis*, *Serratia liquefaciens*, *Morganella morganii*, *Enterobacter cloacae* or *Ruminococcus hydrogenotrophicus*.

*AM 11/9/07* *24* Please amend the paragraph beginning at page 23, line 1, as follows:

Figures 4 to 6 show a specificity detection as a function of the organisms, although some crosshybridization reactions may exist. These reactions may be reduced by choosing probes which are shorter and located among the hypervariable intergenic sequences, as